

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: February 16, 2004, 07:11:18 (Search time 81 Seconds)

1318.700 Million cell updates/sec

Title: US-09-684-725-2

Perfect score: 1263

Sequence: 1 MEKLQNASWVQKLEDPFQ.....LLPMTVISLVYLMALRVS I 242

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DB=Issued Patents NA -QFMT=fastp -SURF=p2n.rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:*
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PTCUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1252	99.1	1248	US-09-545-944-1	Sequence 1, Appli
2	680.5	53.9	1212	US-09-170-496D-113	Sequence 113, App
3	680.5	53.9	1212	US-09-170-496D-223	Sequence 223, App
4	677.5	53.6	1535	US-09-668-680-12	Sequence 12, Appl
5	325.5	25.8	4080	US-09-016-434-1346	Sequence 1346, Ap
6	281	22.2	1529	US-08-858-876A-3	Sequence 3, Appli
7	281	22.2	1529	US-09-472-880-3	Sequence 3, Appli
8	277	21.9	1088	US-09-077-675A-6	Sequence 6, Appli
9	277	21.9	1088	US-09-077-674-6	Sequence 6, Appli
10	277	21.9	1101	US-09-016-434-1148	Sequence 1148, Ap
11	277	21.9	1101	US-09-170-496D-87	Sequence 87, Appl
12	277	21.9	1101	US-09-170-496D-209	Sequence 209, App

13	277	21.9	1122	3	US-09-077-675A-9	Sequence 9, Appli
14	277	21.9	1122	4	US-09-077-674-9	Sequence 9, Appli
15	274	21.7	1063	3	US-09-077-675A-1	Sequence 1, Appli
16	274	21.7	1063	3	US-09-077-674-1	Sequence 1, Appli
17	274	21.7	1092	3	US-09-077-675A-15	Sequence 15, Appl
18	274	21.7	1092	4	US-09-077-674-15	Sequence 15, Appl
19	274	21.7	3129	3	US-09-077-675A-14	Sequence 14, Appl
20	274	21.7	3129	4	US-09-077-674-14	Sequence 14, Appl
21	273	21.6	1029	3	US-09-077-675A-4	Sequence 4, Appli
22	273	21.6	1029	4	US-09-077-674-4	Sequence 4, Appli
23	270	21.4	1752	1	US-07-629-1041-1	Sequence 2, Appli
24	269	21.3	1182	1	US-07-629-1041-2	Sequence 2, Appli
25	264	20.9	936	2	US-08-288-663A-13	Sequence 13, Appl
26	264	20.9	1228	2	US-08-288-663A-3	Sequence 3, Appli
27	264	20.9	1229	4	US-09-016-434-1428	Sequence 1428, Ap
28	259	20.5	1194	2	US-08-288-663A-2	Sequence 2, Appli
29	258	20.4	1575	3	US-08-858-876A-1	Sequence 1, Appli
30	258	20.4	1575	3	US-09-472-880-1	Sequence 1, Appli
31	256.5	20.3	2160	3	US-08-188-275A-1	Sequence 1, Appli
32	256.5	20.3	2162	4	US-09-351-198-1	Sequence 1, Appli
33	256.5	20.3	2162	4	US-09-113-426-1	Sequence 1, Appli
34	256.5	20.3	2162	4	US-09-016-434-1379	Sequence 1379, Ap
35	256.5	20.3	2162	4	US-09-355-709C-7	Sequence 7, Appli
36	256	20.3	1542	4	US-09-761-962A-4	Sequence 4, Appli
37	255	20.2	1334	4	US-09-761-962A-3	Sequence 3, Appli
38	255	20.2	1346	4	US-09-761-962A-12	Sequence 12, Appl
39	255	20.2	1355	4	US-09-761-962A-11	Sequence 11, Appl
40	255	20.2	1423	4	US-09-761-962A-1	Sequence 1, Appli
41	255	20.2	1610	4	US-09-761-962A-16	Sequence 16, Appl
42	255	20.2	1729	4	US-09-761-962A-9	Sequence 9, Appli
43	255	20.2	2045	4	US-09-761-962A-10	Sequence 10, Appl
44	253.5	20.1	1610	3	US-08-889-108-7	Sequence 7, Appli
45	253.5	20.1	1610	5	PCT-US94-10358-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-545-944-1
; Sequence 1, Application US/09545944
; Patent No. 6461836
; GENERAL INFORMATION:
; APPLICANT: AMES, ROBERT
; APPLICANT: ELISHOURBAGY, NABIL
; APPLICANT: MICHALOVICH, DAVID
; APPLICANT: SARAU, HENRY
; APPLICANT: SHABON, USMAN
; APPLICANT: VAWTER, LISA
; TITLE OF INVENTION: MOLECULAR CLONING OF A 7TM RECEPTOR
; FILE OF INVENTION: GP70657-1
; FILE REFERENCE: GP70657-1
; CURRENT APPLICATION NUMBER: US/09/545,944
; CURRENT FILING DATE: 2000-04-10
; PRIOR APPLICATION NUMBER: US 09/435,384
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1248
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-545-944-1

Alignment Scores:	1,07e-136	Length:	1248
Pred. No.:	1250.00	Matches:	239
Score:	100.00%	Conservative:	1
Best local Similarity:	99.58%	Mismatches:	0
Query Match:	99.13%	Indels:	0
DB:	4	Gaps:	0

US-09-684-725-2 (1-242) x US-09-545-944-1 (1-1248)


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US-09-170-496D-223
Alignment Scores:
Pred. No.: 5,38e-70 Length: 1212
Score: 680.50 Matches: 126
Percent Similarity: 74.67% Conservative: 42
Best Local Similarity: 56.00% Mismatches: 54
Query Match: 53.88% Indels: 3
DB: 4 Gaps: 2

US-09-684-725-2 (1-242) x US-09-170-496D-223 (1-1212)
QY 17 AspProPheGlnLysHisLeuAsnSerThrGluGluTyrLeuAlaPhe---LeuCysGly 35
DB 37 GACCCT-----GAGGACTTGAACCTGACTGACGAGGCACTGAGACTCAAGTACCTGGGG 90
QY 36 ProArgArgSerHisPhePheLeuProValSerValTyrValProIlePheValVal 55
DB 91 CCCAGCAGCAGAGAGCTGTTTCATGCCCATCTGTGCCACATACCTGCTGCTGCTGGTG 150
QY 56 GlyValIleGlyAsnValLeuValCysLeuValIleLeuGlnHisGlnAlaMetLysThr 75
DB 151 GCGCTGTGGGCAATGGGCTGACCTGTCTGGTCACTCTGCGCCACAGGCCATGCGCAG 210
QY 76 ProThrAsnTyrTyrLeuPheSerLeuAlaValSerAspLeuLeuValLeuLeuGly 95
DB 211 CCTACCAACTACTACTCTTCAGCCTGGCGGTGCGACCTGCTGCTGCTGGTGGGC 270
QY 96 MetProLeuGluValTyrGluMetTyrArgAsnTyrProPheLeuPheGlyProValGly 115
DB 271 CTGCCCTCGAGCTCATGAGATGTGGCACAACCTACCCCTCTCTGCGGCTTGGTGGC 330
QY 116 CysTyrPheLysThrAlaLeuPheGluThrValCysPheAlaSerIleLeuSerIleThr 135
DB 331 TGCTATTTCGACGCTACTGTTTGAGATGGTCTGCTGCGCTCAGTGTCAACGTCCT 390
QY 136 ThrValSerValGluArgTyrValAlaIleLeuHisProPheArgAlaLysLeuGlnSer 155
DB 391 GCCTGAGGTGGAAGCTATATGGCGGTGGTGACCCACTCAGGCCAGGTCCATGGTG 450
QY 156 ThrArgArgAlaLeuArgIleLeuGlyIleValTyrGlyPheSerValLeuPheSer 175
DB 451 ACGGGGCCCATGTGCGCGAGTGTGGGCGGTCTGGGCGGTCTGGCCATGCTCTGCTCC 510
QY 176 LeuProAsnThrSerIleHisGlyIleLysPheHisTyrPheProAsnGlySerLeuVal 195
DB 511 CTGCCCAACACCACTGTCAGCGCATCCGCGAGCTGCAGTGCCTGCGGGGGCCCAAGTG 570
QY 196 ProGlySerAlaThrCysThrValIleLysProMetTyrIleTyrAsnPheIleGln 215
DB 571 CCAGACTCAGCTTTTGCATGTGTGGTCCGCGCCACGCGGCCCTCTACAAATGATGTCAG 630
QY 216 ValThrSerPheLeuPheTyrLeuLeuProMetThrValIleSerValLeuTyrTyrLeu 235
DB 631 ACCACGGCGTGTCTTCTCTGCTGCGCCATGGCCATCATGAGCGTGTCTACCTGCTC 690
QY 236 MetAlaLeuArgVal 240
DB 691 ATTGGGCTGGGACTG 705

RESULT 4
US-09-668-680-12
; Sequence 12, Application US/09668680
; Patent No. 6436703
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Zhou, Ping
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Xue, Aidong J.
; APPLICANT: Xu, Chongjun

; APPLICANT: Dmanac, Radoje T.
; TITLE OF INVENTION: No. 6436703el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 790CIP2A
; CURRENT APPLICATION NUMBER: US/09/668,680
; CURRENT FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: pt_fl_genes Version 2.0
; SEQ ID NO 12
; LENGTH: 1535
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1338)
US-09-668-680-12
Alignment Scores:
Pred. No.: 1.7e-69 Length: 1535
Score: 677.50 Matches: 126
Percent Similarity: 74.22% Conservative: 41
Best Local Similarity: 56.00% Mismatches: 55
Query Match: 53.64% Indels: 3
DB: 4 Gaps: 2

US-09-684-725-2 (1-242) x US-09-668-680-12 (1-1535)
QY 17 AspProPheGlnLysHisLeuAsnSerThrGluGluTyrLeuAlaPhe---LeuCysGly 35
DB 163 GACCCT-----GAGGACTTGAACCTGACTGACGAGGCACTGAGACTCAAGTACCTGGGG 216
QY 36 ProArgArgSerHisPhePheLeuProValSerValTyrValProIlePheValVal 55
DB 217 CCCAGCAGCAGAGAGCTGTTTCATGCCCATCTGTGCCACATACCTGCTGCTGCTGGTG 276
QY 56 GlyValIleGlyAsnValLeuValCysLeuValIleLeuGlnHisGlnAlaMetLysThr 75
DB 277 GCGCTGTGGCAATGGGCTGACCTGTCTGCTCATCTGCGCCACAGGCCATGCGCAGC 336
QY 76 ProThrAsnTyrTyrLeuPheSerLeuAlaValSerAspLeuLeuValLeuLeuGly 95
DB 337 CCTACCAACTACTACTCTTCAGCCTGGCGGTGTCGACCTGCTGCTGCTGCTGGTGGC 396
QY 96 MetProLeuGluValTyrGluMetTyrArgAsnTyrProPheLeuPheGlyProValGly 115
DB 397 CTGCCCTGAGCTCATGAGATGTGGCACAACCTACCCCTCTCTGCTGGCGGTGGTGGC 456
QY 116 CysTyrPheLysThrAlaLeuPheGluThrValCysPheAlaSerIleLeuSerIleThr 135
DB 457 TGCTATTTCGACGCTACTGTTTGAGATGGTCTGCTGCGCTCAGTGTCTCAAGTCACT 516
QY 136 ThrValSerValGluArgTyrValAlaIleLeuHisProPheArgAlaLysLeuGlnSer 155
DB 517 GCCCTGAGCGTGGAAACGCTATGTGGCGGTGTGACCCACTCCAGGCCAGTCCATGGTG 576
QY 156 ThrArgArgAlaLeuArgIleLeuGlyIleValTyrGlyPheSerValLeuPheSer 175
DB 577 ACGGGGGCCCATGTGCGCGAGTGTCTGGGCGGTCTGGGGGTCTTGGCATGCTCTGCTCC 636
QY 176 LeuProAsnThrSerIleHisGlyIleLysPheHisTyrPheProAsnGlySerLeuVal 195
DB 637 CTGCCCAACACCACTGTCAGCGCATCCGCGAGCTGCAGTGCCTGCGGGGGCCCAAGTG 696
QY 196 ProGlySerAlaThrCysThrValIleLysProMetTyrIleTyrAsnPheIleGln 215
DB 697 CCAGACTCAGCTGTTTGCATGTGTGCCCGCCCGCGGCGCTCTACAAATGATGTCAG 756
QY 216 ValThrSerPheLeuPheTyrLeuLeuProMetThrValIleSerValLeuTyrTyrLeu 235
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Db 757 ACCACGGCGCTCTTCTTCTGCTGCTGCCATGAGCGGTCTCTACCTGCTC 816
Qy 236 MetAlaLeuArgVal 240
Db 817 ATGGGCTCGGACTG 831
RESULT 5
US-09-016-434-1346
; Sequence 1346, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1346:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4080 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g35020
; US-09-016-434-1346
Alignment Scores:
Pred. No.: 8,74e-28 Length: 4080
Score: 325.50 Matches: 86
Percent Similarity: 51.14% Conservative: 49
Best Local Similarity: 32.58% Mismatches: 76
Query Match: 25.77% Indels: 53
DB: 4 Gaps: 10
US-09-684-725-2 (1-242) x US-09-016-434-1346 (1-4080)
Qy 17 AspProPheGlnLysHisLeuAenSerThrGluGluTyrLeu----- 30
Db 421 GACCCCTTCAGCGGGCGGAGCGGCTGCTGGCCCGGGCTTCGGC 480
Qy 31 -----AlaPheLeuCysGlyProArgArgSer----- 39
Db 481 AACGCTTCGGCAACGGCTCGGAGCGGTCTGCGCGCACCCAGCAGCGTGGACGTG 540
Qy 40 -----HisPhePheLeuProValSerValValTyrValProPheVal 55

Db 541 AACACCGCATCTACTCCAAAGTGTGGTGACCGCGGTACTCGCGCTCTCTGGTG 600
Qy 56 GlyValIleGlyAsnValLeuValCysLeuValIleLeuGlnHis-----GlnAla 72
Db 601 GGCACGGTGGCAACACACGGGTGACGGGTTTCACGTGGCGCGGAGAGCGTGCAGAGC 660
Qy 73 MetLysThrProThrAsnTyrTyrLeuPheSerLeuAlaValSerAspLeuValLeu 92
Db 661 CTGCAGACGACGGTGCATTACCACTGGCGACCTGGCGCTGCTCCGACCTGTCACTCG 720
Qy 93 LeuLeuGlyMetProLeuGluValTyrGlu---MetTyrArgAsnTyrProPheLeuPhe 111
Db 721 CTGCTGGCATGCGGCTGGAGCTGTACAACTCACTGGGTGCACACCCCTGGGCGCTTC 780
Qy 112 GlyProValGlyCys-----TyrPheLysThrAlaLeuPheLysValCysPhe 128
Db 781 GGCAGCGCGGCTGCGCGGTACTACTTC-----CTGGCGACGCGCTGCACCTAC 831
Qy 129 AlaSerIleLeuSerIleThrThrValSerValGluArgTyrValAlaIleLeuHisPro 148
Db 832 GCCACGGCCTCAACGTCGCGACCTGAGTGTGGAGCGCTACTGCGCATCTGCCACCCC 891
Qy 149 PheArgAlaLysLeuGlnSerThrArgArgAlaLeuArgIleLeuGlyIleValTyr 168
Db 892 TTCAGGCCCAAGACCTCATGTCCCGAAGCGCACCAAGAGTTTCATCAGCGCATCTCG 951
Qy 169 GlyPheSerValLeuPheSerLeuPro-----AsnThrSer 180
Db 952 CTGCTCGGCGCTGCTGAGCGGTCTATGCTGTTCACCATGGCGGAGCAGACCGCAGC 1011
Qy 181 IleHisGlyIleLysPheHisTyrPheProAsnGlySerLeuVal-----ProGlySer 198
Db 1012 GCCGACGGCCAGCAC-----GCCGGCGGCGCTGTGTGTGCACCCCGCACCATC 1056
Qy 199 AlaThrCysThrValIleLysProMetTyrIleTyrAsnPheIleIleGlnValThrSer 218
Db 1057 CACACTGCCACCGTC-----AAGTGTGTATACAGGTCAACACACC 1095
Qy 219 PheLeuPheTyrLeuLeuProMetThrValIleSerValLeuTyrTyrLeuMetAlaLeu 238
Db 1096 TTCATGTCTTCATATTCCTCCCATGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1155
Qy 239 ArgValSerIle 242
Db 1156 AAGCTGACCGTC 1167
RESULT 6
US-08-858-876A-3
; Sequence 3, Application US/08858876A
; Patent No. 6022856
; GENERAL INFORMATION:
; APPLICANT: Daniel CAPUT
; APPLICANT: Pascale CHALON
; APPLICANT: Pascual FERRARA
; APPLICANT: Vita NATALIO
; TITLE OF INVENTION: Type 2 Neurotensin Receptor
; TITLE OF INVENTION: (Int-R2)
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern, PLLC
; STREET: 400 Seventh Street
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/858,876A

FILING DATE: 19-SEP-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA: PCT/FR 9723204
APPLICATION NUMBER: PCT/FR 9723204
FILING DATE: 17-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,049
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1529 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Rat
FEATURE:
NAME/KEY: CDS
LOCATION: 41..1288
US-08-858-876A-3

Alignment Scores:
Pred. No.: 3,29e-23 Length: 1529
Score: 281.00 Matches: 72
Percent Similarity: 54.90% Conservative: 40
Best Local Similarity: 35.29% Mismatches: 78
Query Match: 22.25% Indels: 14
DB: 3 Gaps: 6

US-09-684-725-2 (1-242) x US-08-858-876A-3 (1-1529)

QY 46 SerValValTyrValProIlePheValValGlyValIleGlyAsnValLeuValCysLeu 65
DB 146 ACCGGCTCTACTCGCTCATCTTCGATTTGGACACAGCGGCAATGCGCTGCCGTGCAC 205
QY 66 ValIleLeuGlnHisGlnAlaMetLysThr---ProThrAsnTyrTyrLeuPheSerLeu 84
DB 206 GTGGTCTGAAGCGCGCGCGCTGCCCGGGCGCTCGCTACACAGCTGCTCAGCTG 265
QY 85 AlaValSerAspLeuLeuValLeuLeuLeuMetProLeuGluValTyrGlu---Met 103
DB 266 GCGCTCTACGCTCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 325
QY 104 TrpArgAsnTyrProPheLeuPheGlyProValGlyCys-----TyrPheLysThr 120
DB 326 TGGTCCCACTACCAATGGGCTTCGCGCATCTGGGCTGCGCTGCTGCTGCTGCTGCTGCTG 379
QY 121 AlaLeuPheGluThrValCysPheAlaSerIleLeuSerIleThrThrValSerValGlu 140
DB 380 ---GTGCGGAGCTGTGCGCTTACGCCACAGTGTGCGGCTGCGGCTGCGGCTGCGGCTGCG 436
QY 141 ArgTyrValAlaIleLeuHisProPheArgAlaLysLeuGlnSerThrArgArgAla 160
DB 437 CGTGTGCTGCGGCTGTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCG 496
QY 161 LeuArgIleLeuGlyIleValTrpGlyPheSerValLeuPheSerLeuProAsnThrSer 180
DB 497 CGCGCTGCTGTCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 556
QY 181 IleHisGlyIleLysPheHisTyr---PheProAsnGlySerLeuValProGlySerAla 199
DB 557 ATCATGGACAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 616
QY 200 ThrCysThrValIleLysProMetTrpIleTyrAsnPheIleIleGlnValThrSerPhe 219
DB 617 GTGTGCGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 676
QY 220 LeuPheTyrLeuLeuProMetThrValIleSerValLeu-----TyrTyr 234
DB 677 GTGTCTCTGCT 736
QY 235 LeuMetAlaLeu 238

Db 737 CTGATGCCCTC 748

RESULT 7
US-09-472-880-3
Sequence 3, Application US/09472880
Patent No. 6274333
GENERAL INFORMATION:
APPLICANT: Daniel CAPUT
Pascual CHALON
Vita NATALIO
TITLE OF INVENTION: Type 2 Neurotensin Receptor (hNT-R2)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern, PLLC
STREET: 400 Seventh Street
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09472,880
FILING DATE: 28-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 9723204
FILING DATE: 17-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,049
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1529 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Rat
FEATURE:
NAME/KEY: CDS
LOCATION: 41..1288
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-472-880-3

Alignment Scores:
Pred. No.: 3,29e-23 Length: 1529
Score: 281.00 Matches: 72
Percent Similarity: 54.90% Conservative: 40
Best Local Similarity: 35.29% Mismatches: 78
Query Match: 22.25% Indels: 14
DB: 3 Gaps: 6

US-09-684-725-2 (1-242) x US-09-472-880-3 (1-1529)

QY 46 SerValValTyrValProIlePheValValGlyValIleGlyAsnValLeuValCysLeu 65
DB 146 ACCGGCTCTACTCGCTCATCTTCGATTTGGACACAGCGGCAATGCGCTGCCGTGCAC 205
QY 66 ValIleLeuGlnHisGlnAlaMetLysThr---ProThrAsnTyrTyrLeuPheSerLeu 84
DB 206 GTGGTCTGAAGCGCGCGCGCTGCCCGGGCGCTCGCTACACAGCTGCTCAGCTG 265
QY 85 AlaValSerAspLeuLeuValLeuLeuLeuMetProLeuGluValTyrGlu---Met 103
DB 266 GCGCTCTACGCTCTGCTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 325

QY 104 TrpArgAsnTyrProPheLeuPheGlyProValGlyCys-----TyrPheLysThr 120
Db 326 TGGTCCCACTACCCATGGGTCTTCGGCGATCTGGGCTGCGGTGATTAATCTTC----- 379
QY 121 AlaLeuPheGluThrValCysPheAlaSerIleLeuSerIleThrThrValSerValGlu 140
Db 380 --GTGCGGAGCTGTGCGCCCTACGCCACAGTGTGAGCGTTGCCAGCTTAAGCGCAGAG 436
QY 141 ArgTyrValAlaIleLeuHisProPheArgAlaLysLeuGlnSerThrArgArgAla 160
Db 437 CGTGCTGCTGGCGTGGCGAGCGGTGCGCGCGCGCGCTTCTACCGCGCGCGCACC 496
QY 161 LeuArgIleLeuGlyIleValTrpGlyPheSerValLeuPheSerLeuProAsnThrSer 180
Db 497 CGCGGCTGTGTCACTGTGTGGTGGTCTCTCTGGGCTTGGCCCTGCCCATGCGGTT 556
QY 181 IleHisGlyLysPheHisTyr---PheProAsnGlySerLeuValProGlySerAla 199
Db 557 ATCATGGACAGAACGACGAGTGAAGCGCGGAGCGGAGCGCTGAGCTTGCCTCGCGT 616
QY 200 ThrCysThrValIleLysProMetTyrIleTyrAsnPheIleIleGlnValThrSerPhe 219
Db 617 GTGTGACAGTGTGTGAGCGCGCGCCACACTTCAAGTCTTATCAGGTGAATGTGTG 676
QY 220 LeuPheTyrLeuLeuProMetThrValIleSerValLeu-----TyrTyr 234
Db 677 GTGTCTTGGCTTCCCTTGGACACTCACTGTTCTTCTGAATGGCATCACTGTCAACAC 736
QY 235 LeuMetAlaLeu 238
Db 737 CTGATGCGCCTC 748

RESULT 8

US-09-077-675A-6
; Sequence 6, Application US/09077675A
; Patent No. 6242199
; GENERAL INFORMATION:
; APPLICANT: Pai, Lee-Yuh
; APPLICANT: Feighner, Scott C.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Pong, Sheng-Shung
; APPLICANT: Van Der Ploeg, Leonardus H.T.
; TITLE OF INVENTION: RECEPTOR ASSAY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,675A
; FILING DATE: 3-JUN-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cocuzzo, Anna L.
; REGISTRATION NUMBER: 42,452
; REFERENCE/DOCKET NUMBER: 19590P
; TELEPHONE: 732-594-1273
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 1088 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-077-675A-6

Alignment Scores:

Pred. No.: 5,88e-23 Length: 1088
Score: 277.00 Matches: 66
Percent Similarity: 54.33% Conservative: 47
Best Local Similarity: 31.73% Mismatches: 69
Query Match: 21.93% Indels: 26
DB: 3 Gaps: 5

US-09-684-725-2 (1-242) x US-09-077-675A-6 (1-1088)

QY 45 ValSerValValTyrValProIlePheValValGlyValIleValAsnValLeuValCys 64
Db 123 GTCACAGCCACCTGCGTGGCACTCTTCGTGGTGGGTATCGCTGGCAACCTGCTCCACATG 182
QY 65 LeuValIleLeuGlnHisGlnAlaMetLysThrProThrAsnTyrTyrLeuPheSerLeu 84
Db 183 CTGTGTGTGCGGCTTCCGCGAGCTGGCAGCCACCACTCTACTCTGTCTCCAGCATG 242
QY 85 AlaValSerAspLeuLeuValLeuLeuGlyMetProLeuGluValTyrGluMetTrp 104
Db 243 GCCTTCTCCGATCTGCTCATCTTCTCTGC---ATGCCCTGGACCTCGTTCGCTCTCG 299
QY 105 ArgAsnTyrProPheLeuPheGlyProValGlyCysTyrPheLysThrAlaLeuPheGlu 124
Db 300 CAGTACCGGCGCTGGAACCTTCGGCGACCTCTCTGCAAACTCTTCCAACTTCGTCAGTGAG 359
QY 125 ThrValCysPheAlaSerIleLeuSerIleThrThrValSerValGluArgTyrValAla 144
Db 360 AGTGTGACCTACGCCAGCGGTCTACCATCACAGCGCTGAGCGCTGAGCGCTACTTCGCC 419
QY 145 IleLeuHisProPheArgAlaLysLeuGlnSerThrArgArgArgAlaLeuArgIleLeu 164
Db 420 ATCTGTCTCCACTCCGCGGCAAGGTGGTGTGTCACCAAGGGGGGGTGAAGCTGTCATC 479
QY 165 GlyIleValTrpGlyPheSerValLeuPheSerLeuProAsnThrSerIleHisGlyIle 184
Db 480 TTCGTATCTGGCGCGTGGCTTCTGCGAGCGCGCGGCCCATCTTCGTGTAGTTCGGGGTG 539
QY 185 LysPheHisTyrPheProAsnGlySer----- 193
Db 540 GAGCACGAG-----AACGGCACCGACCTTGGGACACCAACGAGTCCGCCCCOACC 590
QY 194 --LeuValProGlySerAlaThrCysThrValIleLysProMetTyrIleTyrAsnPhe 212
Db 591 GAGTTTGGGTGGCTCTGAGCTGCTCAGGTGATG-----GTGGGGTG----- 635
QY 213 IleIleGlnValThrSerPheLeuPheTyrLeuLeuProMetThrValIleSerValLeu 232
Db 636 -----TCCAGCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 680
QY 233 TyrTyrLeuMetAlaLeuArgVal 240
Db 681 TACAGTCTCATCGGCGAGGAGCTG 704

RESULT 9

US-09-077-674-6
; Sequence 6, Application US/09077674
; Patent No. 6531314
; GENERAL INFORMATION:
; APPLICANT: Arena, Joseph P.
; APPLICANT: Cully, Doris F.
; APPLICANT: Feighner, Scott D.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Liberator, Paul A.
; APPLICANT: Schaeffer, James M.

Query Match:	21.93%	Indels:	26
DB:	4	Gaps:	5
US-03-684-725-2 (1-242) x US-09-016-434-1148 (1-1101)			

[illegible]

RESULT 11
 US-09-170-496D-87
 ; Sequence 87, Application US/09170496D
 ; Patent No. 6555339
 ; GENERAL INFORMATION:
 ; APPLICANT: Behan, Dominic P.
 ; APPLICANT: Chalmers, Derek T.
 ; APPLICANT: Liaw, Chen W.
 ; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
 ; TITLE OF INVENTION: Receptors
 ; FILE REFERENCE: AREN-0040
 ; CURRENT APPLICATION NUMBER: US/09/170,496D
 ; CURRENT FILING DATE: 1998-10-13
 ; NUMBER OF SEQ ID NOS: 294
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 87
 ; LENGTH: 1101
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-170-496D-87

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Alignment Scores:
Pred. No.:      5.98e-23
Score:          277.00
Length:         1101
Matches:        66

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Percent Similarity:	54.33%	Conservative:	47
Best Local Similarity:	31.73%	Mismatches:	69
Query Match:	21.93%	Indels:	26
DB:	4	Gaps:	5

US-09-684-725-2 (1-242) x US-09-170-496D-87 (1-1101)

[illegible]

RESULT 12
US-09-170-496D-209
: Sequence 209. Application US/09170496D

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/ Patent No. 6555339
/
/ GENERAL INFORMATION:
/
/ APPLICANT: Behan, Dominic P.
/ APPLICANT: Chalmers, Derek T.
/ APPLICANT: Liaw, Chen W.
/
/ TITLE OF INVENTION: No. 6555339-Endogenous
/ TITLE OF INVENTION: Receptors
/ FILE REFERENCE: AREN-0040
/
/ CURRENT APPLICATION NUMBER: US/09/170,496D
/ CURRENT FILING DATE: 1998-10-13
/ NUMBER OF SEQ ID NOS: 294
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 209
/ LENGTH: 1101
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-09-170-496D-209

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Alignment Scores:


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Pred. No.: 5.98e-23 Length: 1101
Score: 277.00 Matches: 66
Percent Similarity: 54.33% Conservative: 47
Best Local Similarity: 31.73% Mismatches: 69
Query Match: 21.93% Indels: 26
DB: 4 Gaps: 5

US-09-684-725-2 (1-242) x US-09-170-496D-209 (1-1101)

QY 45 valserValValTyrValProLeuPheValValGlyValValLeuGlyAsnValValLeuValCys 64
Db 136 GTCACAGCACCTCGCTGCACTCTTCGGTGGTATCGCTGGCAACCTGCTCACCATG 195
QY 65 LeuValLeuGlnHisGlnAlaMetLysThrProThrAsnTyrTyrLeuPheSerLeu 84
Db 196 CTGTGTGTGGCTTCGGAGCTGCGCACACACACCACTTACCTGCTGCGAGCATG 255
QY 85 AlaValSerAspLeuLeuValLeuLeuGlyMetProLeuGluValTyrGluMetTyr 104
Db 256 GCCTTCTCCGATCTGCTATCTTCCTCTGC--ATGCCCTGGACCTGCTGCTCGG 312
QY 105 ArgAsnTyrProPheLeuPheGlyProValGlyCysTyrPheLysThrAlaLeuPheGlu 124
Db 313 CAGTACCGGCTCGGAACCTTCGGCAGCTCTCTGCAAACTCTTCAATTCGTCAGTGAG 372
QY 125 ThrValCysPheAlaSerLeuSerLeuThrValSerValGluArgTyrValAla 144
Db 373 AGCTGACCTACCCAGCTGCTCACCATCAGCGCTGAGCGCTGAGCTGCTGCTG 432
QY 145 IleLeuHisProPheArgAlaLysLeuGlnSerThrArgArgAlaLeuArgIleLeu 164
Db 433 ATCTGTTCCACTTCGGGCCAGGTGGTGGTCCACCAAGGGGGGTGAGTGTGTCATC 492
QY 165 GlyIleValTyrPheSerValLeuPheSerLeuProAsnThrSerIleHisGlyIle 184
Db 493 TTGCTATCTGGCGCTTCTGCGCGCGGCCCTCTCTGCTGCTGCTGCTGCTGCTG 552
QY 185 LysPheHisTyrPheProAsnGlySer----- 193
Db 553 GAGCAGCAG-----AACGGCAGCCAGCTTGGGACACCAACGAGTGGCGCCCCACC 603
QY 194 --LeuValProGlySerAlaThrCysThrValIleLysProMetTyrIleTyrAsnPhe 212
Db 604 GAGTTGGCGTGGCTTGGAGCTGCTCAGCTCATG-----GTGGGGTG----- 648
QY 213 IleIleGlnValThrSerPheLeuPheTyrLeuLeuProMetThrValIleSerValLeu 232
Db 649 -----TCCAGCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 693
QY 233 TyrTyrLeuMetAlaLeuArgVal 240
Db 694 TACAGTCTCATCGGCAGAGAGCTG 717

RESULT 13
US-09-077-675A-9
; Sequence 9, Application US/09077675A
; Patent No. 6242199
; GENERAL INFORMATION:
; APPLICANT: Pai, Lee-Yuh
; APPLICANT: Feighner, Scott C.
; APPLICANT: Howard, Andrew D.
; APPLICANT: Pong, Sheng-Shung
; APPLICANT: Van Der Ploeg, Leonardus H.T.
; TITLE OF INVENTION: RECEPTOR ASSAY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA: US/09/077,675A
APPLICATION NUMBER: US/09-170-496D-209
FILING DATE: 3-JUN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cocuzzo, Anna L.
REGISTRATION NUMBER: 42,452
REFERENCE/DOCKET NUMBER: 19590P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-1273
TELEFAX: 732-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1122 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09-077-675A-9

Alignment Scores:
Pred. No.: 6.15e-23 Length: 1122
Score: 277.00 Matches: 66
Percent Similarity: 54.33% Conservative: 47
Best Local Similarity: 31.73% Mismatches: 69
Query Match: 21.93% Indels: 26
DB: 3 Gaps: 5

US-09-684-725-2 (1-242) x US-09-077-675A-9 (1-1122)

QY 45 ValserValValTyrValProLeuPheValValGlyValValLeuGlyAsnValValLeuValCys 64
Db 388 GTCACAGCACCTCGCTGCGCACCTCTTCGTGGTATCGCTGGCAACCTGCTCACCATG 447
QY 65 LeuValIleLeuGlnHisGlnAlaMetLysThrProThrAsnTyrTyrLeuPheSerLeu 84
Db 448 CTGTGTGTGTGGCTTCGGAGCTGCGCACACACCACTTCTTCAATTCGTCAGTGAG 507
QY 85 AlaValSerAspLeuLeuValLeuLeuGlyMetProLeuGluValTyrGluMetTyr 104
Db 508 GCCTTCTCCGATCTGCTATCTTCCTCTGC---ATGCCCTGGACCTGCTGCTGCTG 564
QY 105 ArgAsnTyrProPheLeuPheGlyProValGlyCysTyrPheLysThrAlaLeuPheGlu 124
Db 565 CAGTACCGGCTCGGAACCTTCGGCAGCTCTCTGCAAACTCTTCCAAATTCGTCAGTGAG 624
QY 125 ThrValCysPheAlaSerIleLeuSerIleThrThrValSerValGluArgTyrValAla 144
Db 625 AGCTGACCTACCCAGCTGCTCACCATCAGCGCTGAGCGCTGAGCTGCTGCTGCTG 684
QY 145 IleLeuHisProPheArgAlaLysLeuGlnSerThrArgArgAlaLeuArgIleLeu 164
Db 685 ATCTGTTCCACTTCGGGCCAGGTGGTGGTCCACCAAGGGGGGTGAGTGTGTCATC 744
QY 165 GlyIleValTyrPheSerValLeuPheSerLeuProAsnThrSerIleHisGlyIle 184
Db 745 TTGCTATCTGGCGCTTCTGCGCGCGGCCCTCTTCTGCTGCTGCTGCTGCTGCTG 804
QY 185 LysPheHisTyrPheProAsnGlySer----- 193
Db 805 GAGCAGCAG-----AACGGCAGCCAGCTTGGGACACCAACGAGTGGCGCCCCACC 855
QY 194 ---LeuValProGlySerAlaThrCysThrValIleLysProMetTyrIleTyrAsnPhe 212
Db 856 GAGTTGGCGTGGCTTGGAGCTGCTCAGCGTCTG-----GTGGGGTG----- 900
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; REGISTRATION NUMBER: 42,452
; REFERENCE/DOCKET NUMBER: 19590P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 732-594-1273
; TELEFAX: 732-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1063 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-077-675A-1

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Alignment Scores:
Pred. No.: 1.27e-22 Length: 1063
Score: 274.00 Matches: 66
Percent Similarity: 54.33% Conservative: 47
Best Local Similarity: 31.73% Mismatches: 69
Query Match: 21.69% Indels: 26
DB: 3 Gaps: 5

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US-09-684-725-2 (1-242) x US-09-077-675A-1 (1-1063)

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Qy 45 valserValValTyrValProIlePheValValGlyValIleGlyAsnValLeuValCys 64
Db 98 GTACCGCCACCTCGCGTGGCGCTTCTGGTGGGTATCGCGGCAACCTGCTCAGATG 157
Qy 65 LeuValIleLeuGlnHisGlnAlaMetLysThrProThrAsnTyrTyrLeuPheSerLeu 84
Db 158 CTGGTAGTGCAGCTTCCCGGAGATGGCGACCAACCACCTCTACTCTCCAGCATG 217
Qy 85 AlaValSerAspLeuLeuValLeuLeuLeuGlyMetProLeuGluValTyrGluMetTrp 104
Db 218 GCCTTCTCCGACCTACTCATCTCTCTGCG--ATGCCCTCGACCTCTTCGCGCTCTGG 274
Qy 105 ArgAsnTyrProPheLeuPheGlyProValGlyCysTyrPheLysThrAlaLeuPheGlu 124
Db 275 CAGTACCGGCTTGGACCTTGGCAACCTCTCTGCAAACTCTTCAGTTCTGTTAGCGAG 334
Qy 125 ThrValCysPheAlaSerIleLeuSerIleThrThrValSerValGluArgTyrValAla 144
Db 335 AGCTGCACCTACGCCACAGTGTCTACCATCCCGCTGAGCGCTGAGCGCTACTTCGCC 394
Qy 145 IleLeuHisProPheArgAlaLysLeuGlnSerThrArgArgAlaLeuArgIleLeu 164
Db 395 ATCTGCTTCCGCTGCGGGCCAGGTAGTGTACCAAGGGCCGGTAAAGCTGGTCATC 454
Qy 165 GlyIleValTrpGlyPheSerValLeuPheSerLeuProAsnThrSerIleHisGlyIle 184
Db 455 CTGTCATCTGGCGCGGCTTCTGTCAGCGCGGCCCATCTTCGTGCTGGTCGGAGTG 514
Qy 185 LysPheHisTyrPheProAsnGlySer-----193
Db 515 GAG-----CATGATAACGGCAGCTGCGGACCAACAGAGTCCGCGCCACG 565
Qy 194 --LeuValProGlySerAlaThrCysThrValIleLysProMetTrpIleTyrAsnPhe 212
Db 566 GAGTTCGCGTGGCGCTCCGGCTGTCTACCGTCAAG-----GTCTGGGG-----610
Qy 213 IleIleGlnValThrSerPheLeuPheTyrLeuLeuProMetThrValIleSerValLeu 232
Db 611 -----TCCAGTGTCTTCTTCTCTGCTGTCTCTGCTCACTGTGCTC 655
Qy 233 TyrTyrLeuMetAlaLeuArgVal 240
Db 656 TATAGCCTCATCGGAGGAAGCTC 679

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Search completed: February 16, 2004, 08:18:52
Job time : 89 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 16, 2004, 08:10:04 ; Search time 325 Seconds

(without alignment)
2742.890 Million cell updates/sec

Title: US-09-684-725-2

Perfect score: 1263

Sequence: 1 MEKLNQASWYQOKLEDPFQ.....LLPMTVISVLYLMALRVS I 242

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2449703 segs, 1841816367 residues

Total number of hits satisfying chosen parameters: 4899406

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:
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15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description

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2	1252	99.1	1239	15	US-10-225-567A-556	Sequence 556, App	
3	1252	99.1	1248	12	US-10-417-820A-11	Sequence 11, Appl	
4	1252	99.1	1248	13	US-10-272-983-11	Sequence 11, Appl	
5	1252	99.1	1248	13	US-10-393-807-11	Sequence 11, Appl	
6	680.5	53.9	1212	13	US-10-353-690-9	Sequence 9, Appl	
7	680.5	53.9	1212	15	US-10-083-168-13	Sequence 13, Appl	
8	680.5	53.9	1212	15	US-10-083-168-82	Sequence 82, Appl	
9	680.5	53.9	1212	15	US-10-251-385-113	Sequence 113, Appl	
10	680.5	53.9	1212	15	US-10-251-385-223	Sequence 223, Appl	
11	680.5	53.9	1212	15	US-10-225-567A-539	Sequence 539, App	
12	680.5	53.9	1212	15	US-10-290-078-16	Sequence 16, Appl	
13	680.5	53.9	1212	15	US-10-290-078-17	Sequence 17, Appl	
14	677.5	53.6	1349	12	US-10-240-145-96	Sequence 96, Appl	
15	677.5	53.6	1335	12	US-10-240-145-10	Sequence 10, Appl	
16	677.5	53.6	1535	15	US-10-146-419-12	Sequence 12, Appl	
17	677.5	53.6	1535	15	US-10-146-419-12	Sequence 12, Appl	
18	418	33.1	1258	9	US-09-804-551B-25	Sequence 25, Appl	
19	418	33.1	1287	15	US-10-270-333-113	Sequence 113, App	
20	418	33.1	4314	15	US-10-270-333-112	Sequence 112, App	
21	352	27.9	1788	15	US-10-270-333-194	Sequence 194, App	
22	338	26.8	1293	12	US-10-157-317-160	Sequence 160, App	
23	338	26.8	1293	12	US-10-157-339-160	Sequence 160, App	
24	338	26.8	1293	13	US-10-157-305A-160	Sequence 160, App	
25	338	26.8	1293	13	US-10-157-391-160	Sequence 160, App	
26	338	26.8	1293	13	US-10-157-096-160	Sequence 160, App	
27	338	26.8	1293	13	US-10-157-215A-160	Sequence 160, App	
28	338	26.8	1293	13	US-10-157-302-160	Sequence 160, App	
29	338	26.8	1293	13	US-10-154-951B-160	Sequence 160, App	
30	338	26.8	1293	13	US-10-157-299-160	Sequence 160, App	
31	338	26.8	1293	13	US-10-156-831-160	Sequence 160, App	
32	338	26.8	1293	13	US-10-156-902-160	Sequence 160, App	
33	338	26.8	1293	13	US-10-157-147-160	Sequence 160, App	
34	338	26.8	1293	13	US-10-157-166-160	Sequence 160, App	
35	338	26.8	1293	13	US-10-157-318-160	Sequence 160, App	
36	338	26.8	1293	13	US-10-156-811-160	Sequence 160, App	
37	338	26.8	1293	13	US-10-157-320A-160	Sequence 160, App	
38	338	26.8	1293	13	US-10-157-418A-160	Sequence 160, App	
39	338	26.8	1626	12	US-10-157-317-162	Sequence 162, App	
40	338	26.8	1626	12	US-10-157-339-162	Sequence 162, App	
41	338	26.8	1626	13	US-10-157-305A-162	Sequence 162, App	
42	338	26.8	1626	13	US-10-157-391-162	Sequence 162, App	
43	338	26.8	1626	13	US-10-157-096-162	Sequence 162, App	
44	338	26.8	1626	13	US-10-157-215A-162	Sequence 162, App	
45	338	26.8	1626	13	US-10-157-302-162	Sequence 162, App	

ALIGNMENTS

RESULT 1

US-09-782-974C-17/c
; Sequence 17, Application US/09782974C
; Publication No. US20030082534A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Lind, Peter
; APPLICANT: Wood, Linda S.
; APPLICANT: Parodi, Luis A.
; TITLE OF INVENTION: No. US20030082534A1 G Protein Coupled Receptor
; FILE REFERENCE: 411USPHRM311
; CURRENT APPLICATION NUMBER: US/09/782.974C
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 60/165,838
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 09/714,449
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/198,568
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,071
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,678
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/173,396

; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/184,129
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/185,421
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/185,554
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/186,530
; PRIOR FILING DATE: 2000-03-02
; Remaining prior application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 801
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-782-974C-17

Alignment Scores:
Pred. No.: 2,58e-139 Length: 801
Score: 1263.00 Matches: 242
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-09-684-725-2 (1-242) x US-09-782-974C-17 (1-801)

QY 1 MetGluLysLeuGlnAsnAlaSerTrpIleTyrGlnGlnLysLeuGluAspProPheGln 20
DB 795 ATGGAAAACCTTCAGATGCTTCTGGATCTACACGAGAACTAGAGATCCATCCAG 736
QY 21 LysHisLeuAsnSerThrGluGluTyrLeuAlaPheLeuGlyCysGlyProArgGSerHis 40
DB 735 AAACACCTGAACAGCCAGGAGTATCTGGCCCTCTCTGGGACCTCGGGCAGCCAC 676
QY 41 PhePheLeuProValSerValValTyrValProIlePheValValGlyValIleGlyAsn 60
DB 675 TTCTTCTCCCGTGTCTGGGTATGTGCGCAATTTTGTGGTGGGGTCTATTGGCAAT 616
QY 61 ValLeuValCysLeuValIleLeuGlnHisGlnAlaMetLysThrProThrAsnTyrTyr 80
DB 615 GTCTGTGTGTCTGTGTATCTGCGAGCACCGAGCTATGAGACGCCACCACTACTAC 556
QY 81 LeuPheSerLeuAlaValSerAspLeuLeuValLeuLeuGlyMetProLeuGluVal 100
DB 555 CTCTTCAGCCTGGCGGTCTCTGACCTCTGCTCTCTCTCTGGAATGCGCTGGAGGTC 496
QY 101 TyrGluMetTrpArgAsnTyrProPheLeuPheGlyProValGlyCysTyrPheLysThr 120
DB 495 TATGAGATGTGGCGCAACTACCCCTTTCTGTTCGGGCGCGTGGCTGTCTTCAAGAGC 436
QY 121 AlaLeuPheGluThrValCysPheAlaSerIleLeuSerIleThrThrValSerValGlu 140
DB 435 GCCTCTTTGAGACCGGTGTCTTGGCTCTCATCTCAGCATCACCACTGAGCGTGGAG 376
QY 141 ArgTyrValAlaIleLeuHisProPheArgAlaLysLeuGlnSerThrArgArgAla 160
DB 375 CGTACTGTGGCCATCTCTACACCGTTCGGCGCCAACTGCAGAGCACCGGGCGCGGCC 316
QY 161 LeuArgIleLeuGlyIleValTrpGlyPheSerValLeuPheSerLeuProAsnThrSer 180
DB 315 CTGAGGATCTCGCATGCTGTGGGCTTCTCGTGTCTCTCTCTCTCTCTCTCTCTCTCT 256
QY 181 IleHisGlyIleLysPheHisTyrPheProAsnGlySerLeuValProGlySerAlaThr 200
DB 255 ATCCATGGCATCAAGTTCCTACTACTTCCCAATTTGGGTGCTGTGTGTGTGTGTGTGT 196
QY 201 CysThrValIleLysProMetTrpIleTyrAsnPheIleIleGlnValThrSerPheLeu 220
DB 195 TGTACGGTATCAAGCCCATGTGGATCTCAATTTATCATATCAGGTCTACCTCTTCTCTTA 136
QY 221 PheTyrLeuLeuProMetThrValIleSerValLeuTyrTyrLeuMetAlaLeuArgVal 240

DB 135 TTCTACCTCTCCCATGACTGTGCATCACTGTCTCTACTCTACCTCATGGCACTCAGAGTG 76
QY 241 SerIle 242
DB 75 AGTATC 70

RESULT 2

US-10-225-567A-556
; Sequence 556, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glena C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 556
; LENGTH: 1239
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-556

Alignment Scores:
Pred. No.: 9,97e-138 Length: 1239
Score: 1232.00 Matches: 239
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.58% Mismatches: 0
Query Match: 99.13% Indels: 0
DB: 15 Gaps: 0

US-09-684-725-2 (1-242) x US-10-225-567A-556 (1-1239)

QY 1 MetGluLysLeuGlnAsnAlaSerTrpIleTyrGlnGlnLysLeuGluAspProPheGln 20
DB 1 ATGGAAAACCTTCAGATGCTTCTGGATCTACACGAGAACTAGAGATCCATCCAG 60
QY 21 LysHisLeuAsnSerThrGluGluTyrLeuAlaPheLeuGlyCysGlyProArgGSerHis 40
DB 61 AAACACCTGAACAGCCAGGAGTATCTGGCCCTCTCTGGGACCTCGGGCAGCCAC 120
QY 41 PhePheLeuProValSerValValTyrValProIlePheValValGlyValIleGlyAsn 60
DB 121 TTCTTCTCCCGTGTCTGTGTATGTGCGCAATTTTGTGGTGGGGTCTATTGGCAAT 180
QY 61 ValLeuValCysLeuValIleLeuGlnHisGlnAlaMetLysThrProThrAsnTyrTyr 80
DB 181 GTCTGTGTGTCTGTGTATCTGCGACACGAGCTATGAGACGCCACCACTACTAC 240
QY 81 LeuPheSerLeuAlaValSerAspLeuLeuValLeuLeuGlyMetProLeuGluVal 100
DB 241 CTCTTCAGCCTGGCGGTCTCTGACCTCTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
QY 101 TyrGluMetTrpArgAsnTyrProPheLeuPheGlyProValGlyCysTyrPheLysThr 120
DB 301 TATGAGATGTGGCGCAACTACCCCTTTCTGTTCGGGCGCGTGGGCTGTCTACTTCAAGAGC 360
QY 121 AlaLeuPheGluThrValCysPheAlaSerIleLeuSerIleThrThrValSerValGlu 140
DB 361 GCCTCTTTGAGACCGGTGTGTCTGCGCTCTCATCTCTAGCATCACCACTGAGCGTGGAG 420
QY 141 ArgTyrValAlaIleLeuHisProPheArgAlaLysLeuGlnSerThrArgArgAla 160
DB 421 CGCTACGTGGCCATCTCTACACCCCTTCCGCGCCAACTGCAGAGCACCCCGCGCGGCC 480
QY 161 LeuArgIleLeuGlyIleValTrpGlyPheSerValLeuPheSerLeuProAsnThrSer 180

Db 481 CTCAGGATCCTCGGCATGCTCTGGGCTTCTCGGTCTTCTCTCCCTGCCAACACCCAGC 540
 QY 181 IleHisGlyIleLysPheHisTyrPheProAsnGlySerLeuValProGlySerAlaThr 200
 Db 541 ATCCATGGCATCAAGTTCACACTACTTCCCAATGGTCCCTGGTCCAGGTTGGCCACC 600
 QY 201 CysThrValIleLysProMetTrpIleTyrAsnPheIleIleGlnValThrSerPheLeu 220
 Db 601 TGTACGGTCATCAAGCCCATGGATGATCAATTTTCATCATCCAGGTACCTCTTCTCTA 660
 QY 221 PheTyrLeuLeuProMetThrValIleSerValLeuTyrTyrLeuMetAlaLeuArgVal 240
 Db 661 TTCTACCTCTCCCATGACTGTCATCACTGTCCTCTACTACTCTCATGGCACTCAGACTA 720

RESULT 3

US-10-417-820A-11
 ; Sequence 11, Application US/10417820A
 ; Publication No. US20030229216A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, Ruoping
 ; APPLICANT: Liaw, Chen W.
 ; APPLICANT: Lowitz, Kevin
 ; APPLICANT: Chalmers, Derek T.
 ; APPLICANT: Behan, Dominic P.
 ; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled

; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
 ; FILE REFERENCE: 7.US28.CON
 ; CURRENT APPLICATION NUMBER: US/10/417,820A

; CURRENT FILING DATE: 2003-04-16
 ; PRIOR APPLICATION NUMBER: 09/416,760

; PRIOR FILING DATE: 1999-10-12
 ; PRIOR APPLICATION NUMBER: 09/170,496

; PRIOR FILING DATE: 1998-10-13
 ; PRIOR APPLICATION NUMBER: 60/110,060

; PRIOR FILING DATE: 1998-11-27
 ; PRIOR APPLICATION NUMBER: 60/120,416

; PRIOR FILING DATE: 1999-02-16
 ; PRIOR APPLICATION NUMBER: 60/121,852

; PRIOR FILING DATE: 1999-02-26
 ; PRIOR APPLICATION NUMBER: 60/109,213

; PRIOR FILING DATE: 1998-11-20
 ; PRIOR APPLICATION NUMBER: 60/123,944

; PRIOR FILING DATE: 1999-03-12
 ; PRIOR APPLICATION NUMBER: 60/123,945

; PRIOR FILING DATE: 1999-03-12
 ; PRIOR APPLICATION NUMBER: 60/123,948

; PRIOR FILING DATE: 1999-03-12
 ; PRIOR APPLICATION NUMBER: 60/123,951

; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 155

; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 11

; LENGTH: 1248
 ; TYPE: DNA

; ORGANISM: Homo sapiens
 US-10-417-820A-11

Alignment Scores:

Pred. No.: 1,01e-137 Length: 1248

Score: 1252.00 Matches: 239

Percent Similarity: 100.00% Conservative: 1

Best Local Similarity: 99.58% Mismatches: 0

Query Match: 99.13% Indels: 0

DB: 12 Gaps: 0

US-09-684-725-2 (1-242) x US-10-417-820A-11 (1-1248)

QY 1 MetGluLysLeuGlnAsnAlaSerTrpIleTyrGlnGlyLeuGluAspProPheGln 20

Db 10 ATGAAAAAATTCAGATGCTTCTCGATCTACCAAGAACTAGAGATCCATTCCAG 69

QY 21 LysHisLeuAsnSerThrGluTyrLeuAlaPheLeuCysGlyProArgArgSerHis 40
 Db 70 AAACACCTGAACAGACACCGAGGAGTAGTATCTGGCCTTCTCTGCGGACCTCGGCGCAGCCAC 129
 QY 41 PhePheLeuProValSerValValTyrValProIlePheValValGlyValIleGlyAsn 60
 Db 130 TTCTTCTCCCGCTGTCTGTGTGTATGTGTGCAATTTTGTGTGGGGGTTCATTTGGCAAT 189
 QY 61 ValLeuValCysLeuValIleLeuGlnHisGlnAlaMetLysThrProThrAsnTyrTyr 80
 Db 190 GTCTGTGTGTGGTGGTATCTGACGACCGAGCTATGAAGACGCCCACTACTACTAC 249
 QY 81 LeuPheSerLeuAlaValSerAspLeuLeuValLeuLeuLeuGlyMetProLeuGluVal 100
 Db 250 CTCTTCAGCCCTGGCGGTCTCTGACCTCCCTGGTCTCTCTCTGATGATGCCCCCTGGAGGTC 309
 QY 101 TyrGluMetTrpArgAsnTyrProPheLeuPheGlyProValGlyCysTyrPheLysThr 120
 Db 310 TATGAGATGTGGCGCAACTACCTTTCTTGTTCGGGCGCCGTGGGCTGTACTTTCAAGACG 369
 QY 121 AlaLeuPheGluThrValCysPheAlaSerIleLeuSerIleThrThrValSerValGlu 140
 Db 370 GCCCTCTTTCAGACCGGTGTCTTCCCTCCATCCTCAGCATCACCACCGTCAGGTGGAG 499
 QY 141 ArgTyrValAlaIleLeuHisProPheArgAlaLysLeuGlnSerThrArgArgAla 160
 Db 430 CGCTACGTGGCCATCTTACACCCGTTCGGCGCCAACTGCAGAGACCCCGCCGCGGCC 489
 QY 161 LeuArgIleLeuGlyIleValTyrPheSerValLeuPheSerLeuProAsnThrSer 180
 Db 490 CTCAGGATCCTCGGCATCGTCTGGGGCTTCTCGTGTCTCTCTCTCCCTGCCCAACACCCAGC 549
 QY 181 IleHisGlyIleLysPheHisTyrPheProAsnGlySerLeuValProGlySerAlaThr 200
 Db 550 ATCCATGGCATCAAGTTCACACTACTTCCCAATGGGTCCCTGGTCCAGGTTCCGGCCACC 609
 QY 201 CysThrValIleLysProMetTrpIleTyrAsnPheIleIleGlnValThrSerPheLeu 220
 Db 610 TGTACGGTCTATCAAGCCCATGTGATCTCAATTTTCATCATCCAGGTCACCTCTTCTCTA 669
 QY 221 PheTyrLeuLeuProMetThrValIleSerValLeuTyrTyrLeuMetAlaLeuArgVal 240
 Db 670 TTCTACCTCTCCCATGACTGTCTCACTAGTGTCTTACTACTCTATGGCACTCAGACTA 729

RESULT 4

US-10-272-983-11
 ; Sequence 11, Application US/10272983
 ; Publication No. US20030148450A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chen, Ruoping
 ; APPLICANT: Dang, Huong T.
 ; APPLICANT: Liaw, Chen W.
 ; APPLICANT: Lin, I-Lin
 ; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
 ; FILE REFERENCE: AREN0050
 ; CURRENT APPLICATION NUMBER: US/10/272,983
 ; CURRENT FILING DATE: 2002-10-17
 ; PRIOR APPLICATION NUMBER: US/09/417,044
 ; PRIOR FILING DATE: 1999-10-12
 ; PRIOR APPLICATION NUMBER: 60/109,213
 ; PRIOR FILING DATE: 1998-11-20
 ; PRIOR APPLICATION NUMBER: 60/120,416
 ; PRIOR FILING DATE: 1999-02-16
 ; PRIOR APPLICATION NUMBER: 60/121,851
 ; PRIOR FILING DATE: 1999-02-26
 ; PRIOR APPLICATION NUMBER: 60/123,946
 ; PRIOR FILING DATE: 1999-03-12
 ; PRIOR APPLICATION NUMBER: 60/123,949
 ; PRIOR FILING DATE: 1999-03-12
 ; PRIOR APPLICATION NUMBER: 60/136,436
 ; PRIOR FILING DATE: 1999-05-28
 ; PRIOR APPLICATION NUMBER: 60/136,437
 ; PRIOR FILING DATE: 1999-05-28

```
/ PRIOR APPLICATION NUMBER: 60/136,439
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,567
/ PRIOR FILING DATE: 1999-05-28
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 74
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 11
/ LENGTH: 1248
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-272-983-11
Alignment Scores:
Pred. No.: 1,01e-137 Length: 1248
Score: 1252.00 Matches: 239
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.58% Mismatches: 0
Query Match: 99.13% Indels: 0
DB: 13 Gaps: 0
US-09-684-725-2 (1-242) x US-10-272-983-11 (1-1248)
Qy 1 MetGluLysLeuGlnAsnAlaSerTrpIleTyrGlnLysLeuGluAspProPheGln 20
Db 10 ATGGAAAACTTCAGAAATGCTTCTGGATCTACCGACAGAACTAGACATCCATTCCAG 69
Qy 21 LysHisLeuAsnSerThrGluGluTyrLeuAlaPheLeuCysGlyProArgArgSerHis 40
Db 70 AAACACCTGAACACCGAGGAGTATCTGGCTTCTCTGGGACCTCGGCGACCCAC 129
Qy 41 PhePheLeuProValSerValValTyrValProIlePheValValGlyValIleGlyAsn 60
Db 130 TTCTTCTCCCTGCTGCTGGTGTATGTGCAATTTTCTGGTGGGGGTCAATGGCAAT 189
Qy 61 ValLeuValCysLeuValIleLeuGlnHisGlnAlaMetLysThrProThrAsnTyrTyr 80
Db 190 GTCCTGGTGTGCTGGTGTATCTGACGACGAGCTATGAAGACCGCCACCACTACTAC 249
Qy 81 LeuPheSerLeuAlaValSerAspLeuLeuValLeuLeuGlyMetProLeuGluVal 100
Db 250 CTCCTTCAGCTCGGGGTCTCTGACCTCTGCTCTCTCTGCTCTCTGCTCTCTGCTCT 309
Qy 101 TyrGluMetTrpArgAsnTyrProPheLeuPheGlyProValGlyCysTyrPheLysThr 120
Db 310 TATGAGATGGCGCACTACCTCTTCTTCTGGGCGGCTGCTGCTGCTGCTGCTGCTG 369
Qy 121 AlaLeuPheGluThrValCysPheAlaSerIleLeuSerIleThrThrValSerValGlu 140
Db 370 GCCTCTTTGAGACCGGTGCTTGGCTTCCATCTCAGCATCACCATCCGCTGAGGTGAG 429
Qy 141 ArgTyrValAlaIleLeuHisProPheArgAlaLysLeuGlnSerThrArgArgAla 160
Db 430 CGCTACGTGGCCATCTACACCGGTTCCGCGCCAACTGCAGAGCACCGCGCGCGGCC 489
Qy 161 LeuArgIleLeuGlyIleValTrpGlyPheSerValLeuPheSerLeuProAsnThrSer 180
Db 490 CTCAGGATCTCGGCATCGTCTGGGCTTCTCGCTGCTCTCTCTCTCTCTCTCTCTCT 549
Qy 181 IleHisGlyIleLysPheHisTyrPheProAsnGlySerLeuValProGlySerAlaThr 200
Db 550 ATCATGGCATCAAGTTCCTACTTCCCAATGGGTTCCTGCTCCAGTTCGGGCCAC 609
Qy 201 CysThrValIleLysProMetTrpIleTyrAsnPheIleIleGlnValThrSerPheLeu 220
Db 610 TGTACGGTATCATCAAGTTCCTACTTCCCAATGGGTTCCTGCTCCAGTTCGGGCCAC 669
Qy 221 PheTyrLeuLeuProMetThrValIleSerValLeuTyrTyrLeuMetAlaLeuArgVal 240
Db 670 TTCTACCTCTCCCATGACTGTGTCATCAGTGTCTCTACTTACCTCATGCACTCAGACTA 729
RESULT 5
US-10-393-807-11
/ Sequence 11, Application US/10393807
/ Publication No. US20030175891A1
/ GENERAL INFORMATION:
/ APPLICANT: Chen, Ruoping
/ APPLICANT: Dang, Huong T.
/ APPLICANT: Liaw, Chen W.
/ APPLICANT: Lin, I-Lin
/ TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
/ FILE REFERENCE: AREN0050
/ CURRENT APPLICATION NUMBER: US/10/393,807
/ CURRENT FILING DATE: 2003-03-21
/ PRIOR APPLICATION NUMBER: US/09/417,044
/ PRIOR FILING DATE: 1999-10-12
/ PRIOR APPLICATION NUMBER: 60/109,213
/ PRIOR FILING DATE: 1998-11-20
/ PRIOR APPLICATION NUMBER: 60/120,416
/ PRIOR FILING DATE: 1999-02-16
/ PRIOR APPLICATION NUMBER: 60/121,851
/ PRIOR FILING DATE: 1999-02-26
/ PRIOR APPLICATION NUMBER: 60/123,946
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,949
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/136,436
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,437
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,439
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,567
/ PRIOR FILING DATE: 1999-05-28
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 74
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 11
/ LENGTH: 1248
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-393-807-11
Alignment Scores:
Pred. No.: 1,01e-137 Length: 1248
Score: 1252.00 Matches: 239
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.58% Mismatches: 0
Query Match: 99.13% Indels: 0
DB: 13 Gaps: 0
US-09-684-725-2 (1-242) x US-10-393-807-11 (1-1248)
Qy 1 MetGluLysLeuGlnAsnAlaSerTrpIleTyrGlnLysLeuGluAspProPheGln 20
Db 10 ATGGAAAACTTCAGAAATGCTTCTGGATCTACCGACAGAACTAGACATCCATTCCAG 69
Qy 21 LysHisLeuAsnSerThrGluGluTyrLeuAlaPheLeuCysGlyProArgArgSerHis 40
Db 70 AAACACCTGAACACCGAGGAGTATCTGGCTTCTCTGGGACCTCGGCGACCCAC 129
Qy 41 PhePheLeuProValSerValValTyrValProIlePheValValGlyValIleGlyAsn 60
Db 130 TTCTTCTCCCTGCTGCTGGTGTATGTGCAATTTTCTGGTGGGGGTCAATGGCAAT 189
Qy 61 ValLeuValCysLeuValIleLeuGlnHisGlnAlaMetLysThrProThrAsnTyrTyr 80
Db 190 GTCCTGGTGTGCTGGTGTATCTGACGACGAGCTATGAAGACCGCCACCACTACTAC 249
Qy 81 LeuPheSerLeuAlaValSerAspLeuLeuValLeuLeuGlyMetProLeuGluVal 100
Db 250 CTCCTTCAGCTCGGGGTCTCTGACCTCTGCTCTCTCTGCTCTCTGCTCTCTGCTCT 309
Qy 101 TyrGluMetTrpArgAsnTyrProPheLeuPheGlyProValGlyCysTyrPheLysThr 120
Db 310 TATGAGATGGCGCACTACCTCTTCTTCTGGGCGGCTGCTGCTGCTGCTGCTGCTG 369
Qy 121 AlaLeuPheGluThrValCysPheAlaSerIleLeuSerIleThrThrValSerValGlu 140
Db 370 GCCTCTTTGAGACCGGTGCTTGGCTTCCATCTCAGCATCACCATCCGCTGAGGTGAG 429
Qy 141 ArgTyrValAlaIleLeuHisProPheArgAlaLysLeuGlnSerThrArgArgAla 160
Db 430 CGCTACGTGGCCATCTACACCGGTTCCGCGCCAACTGCAGAGCACCGCGCGGCC 489
Qy 161 LeuArgIleLeuGlyIleValTrpGlyPheSerValLeuPheSerLeuProAsnThrSer 180
Db 490 CTCAGGATCTCGGCATCGTCTGGGCTTCTCGCTGCTCTCTCTCTCTCTCTCTCTCT 549
Qy 181 IleHisGlyIleLysPheHisTyrPheProAsnGlySerLeuValProGlySerAlaThr 200
Db 550 ATCATGGCATCAAGTTCCTACTTCCCAATGGGTTCCTGCTCCAGTTCGGGCCAC 609
Qy 201 CysThrValIleLysProMetTrpIleTyrAsnPheIleIleGlnValThrSerPheLeu 220
Db 610 TGTACGGTATCATCAAGTTCCTACTTCCCAATGGGTTCCTGCTCCAGTTCGGGCCAC 669
Qy 221 PheTyrLeuLeuProMetThrValIleSerValLeuTyrTyrLeuMetAlaLeuArgVal 240
Db 670 TTCTACCTCTCCCATGACTGTGTCATCAGTGTCTCTACTTACCTCATGCACTCAGACTA 729
RESULT 5
US-10-393-807-11
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QY 121 AlaLeuPheGluThrValCysPheAlaSerIleLeuSerIleThrThrValSerValGlu 140
Db 370 GGCCTCTTTGAGCGGTGTGCTGCGCTCCCTCCCTCCTCAGCATCACACCGCTCAGCGTGGAG 429
QY 141 ArgTyrValAlaIleLeuHisProPheArgAlaIleLeuGlnSerThrArgArgAla 160
Db 430 CGCTACGTGGCGCATCCTACACCGCTCCGCGCAAACTGCAGACACCGCGCGCGGCC 489
QY 161 LeuArgIleLeuGlyIleValTyrPheSerValLeuPheSerLeuProAsnThrSer 180
Db 490 CTCAGATCCTCGGATGCTGTGGGCTTCCTCCGCTCTCTCTCCGCGCAACACCGCAGC 549
QY 181 IleHisGlyIleLeuPheHisTyrPheProAsnGlySerLeuValProGlySerAlaThr 200
Db 550 ATCCATGTCATCAAGTTCACCTACTTCCCAATGGTCCCTGCTCCCGAGGTTCGCGCAC 609
QY 201 CysThrValIleLeuPheProMetTyrPheIleValLeuGlnValThrSerPheLeu 220
Db 610 TGTACGGTTCATCAAGCCCATGTGGATCTACAAATTTTCATCATCCAGGTCCCTCTCTA 669
QY 221 PheTyrLeuLeuProMetThrValIleSerValLeuTyrTyrLeuMetAlaLeuArgVal 240
Db 670 TTCTACCTCCTCCCATGACTGTATCATGAGTGCCTCTACTACCTCATGGCACTCAGACTA 729

RESULT 6
US-10-353-690-9
; Sequence 9, Application US/10353690
; Publication NO. US20030215840A1
; GENERAL INFORMATION:
; APPLICANT: Logan, Thomas Joseph
; APPLICANT: Chun, Miyoung
; APPLICANT: Galvin, Katherine M.
; APPLICANT: Healy, Aileen
; APPLICANT: Acton, Susan L.
; APPLICANT: Donoghue, Mary
; APPLICANT: Stagliano, Nancy
; APPLICANT: Perodin, Jacquelin
; APPLICANT: Rodrigue-Way, Amelie
; TITLE OF INVENTION: Methods and compositions for treating
; TITLE OF INVENTION: cardiovascular disease using 1682, 6169, 6193, 7771, 14395,
; TITLE OF INVENTION: 29002, 33216, 43726, 69292, 26156, 32427, 2402, 7747, 1720,
; TITLE OF INVENTION: 9151, 60491, 1371, 7077, 33207, 1419, 18036, 16105, 38650,
; TITLE OF INVENTION: 14245, 58848, 1870, 25856, 32394, 3484, 345, 9252, 9135,
; TITLE OF INVENTION: 10532, 18610, 8165, 2448, 2445, 64624, 84237, 9912, 2868,
; TITLE OF INVENTION: 283, 2594, 9464, 17799, 26686, 43848, 32135, 12208, 2914,
; TITLE OF INVENTION: 51130, 19489, 21833, 2917, 59590, 15992, 2094, 2252, 3474,
; TITLE OF INVENTION: 9792, 15400, 1452 or 6585 molecules
; FILE REFERENCE: MPI02-018PIRNMNM
; CURRENT APPLICATION NUMBER: US/10/353,690
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: 60/353,224
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/364,529
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: 60/373,861
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/376,287
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: 60/388,080
; PRIOR FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: 60/390,971
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: 60/394,130
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: 60/394,797
; PRIOR FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: 60/404,904
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: 60/405,450
; PRIOR FILING DATE: 2002-08-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 126

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1212
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-353-690-9
Alignment Scores: 3.32e-70 Length: 1212
Pred. No.: 680.50 Matches: 126
Score: 74.67% Conservat: 42
Percent Similarity: 56.00% Mismatches: 54
Best Local Similarity: 53.88% Indels: 3
Query Match: 13 Gaps: 2
DB: 13
US-09-684-725-2 (1-242) x US-10-353-690-9 (1-1212)
QY 17 AspProPheGlnLysHisLeuAsnSerThrGluGluTyrLeuAlaPhe---LeuCysGly 35
Db 37 GACCCCT-----GAGGACTTGAACCTGACTGACGAGGCACTGAGACTCAAGTACCTGGGG 90
QY 36 ProArgArgSerHisPhePheLeuProValSerValValTyrValProIlePheValVal 55
Db 91 CCCAGACAGACAGAGCTGTTCATGCCCATCTGTGCCACATACCTGCTGATCTCTGTTGGT 150
QY 56 GlyValIleGlyAsnValLeuValCysLeuValIleLeuGlnHisGlnAlaMetIleThr 75
Db 151 GCGCTGTGGCAATGGGCTGACCTGTCTGGTTCATCTCTGCGCCACAGGCCATGGCCAG 210
QY 76 ProThrAsnTyrTyrLeuPheSerLeuAlaValSerAspLeuLeuValLeuLeuGly 95
Db 211 CCTACCAACTACTACTCTTCAGCTTGGCGGTGTGGACCTGCTGCTGTGCTGTGTTGGTGG 270
QY 96 MetProLeuGluValTyrGluMetTyrArgAsnTyrProPheLeuPheGlyProValGly 115
Db 271 CTGCCCCCTGGAGCTCTATGAGATGGGCACAACTACCCCTCTCTGCTGGGCGTGTGTGGC 330
QY 116 CysTyrPheLysThrAlaLeuPheGluThrValCysPheAlaSerIleLeuSerIleThr 135
Db 331 TGTATTTCGACGCTACTGTTTGTAGATGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 390
QY 136 ThrValSerValGluArgTyrValAlaIleLeuHisProPheArgAlaLysLeuGlnSer 155
Db 391 GCGCTGAGGTGGCAACGCTATGTGGCGGTGGTGCACCCACTCCAGGCCAGGTCCATGGTG 450
QY 156 ThrArgArgAlaLeuArgIleLeuGlyIleValTyrGlyPheSerValLeuPheSer 175
Db 451 ACGGGGGCCCATGTGGCGCGAGTGTGTGGGGCGGTCTGGGGGTCTTGGCCATGCTCTGCTCC 510
QY 176 LeuProAsnThrSerIleHisGlyIleLysPheHisTyrPheProAsnGlySerLeuVal 195
Db 511 CTGCCCCAACACACCGCTGCACCGGCATCCGCGCAGCTGCAGTCCCTGCGGGGCCCGAGTG 570
QY 196 ProGlySerAlaThrCysThrValIleLysProMetTyrIleTyrAsnPheIleLeuGln 215
Db 571 CGAGACTCAGCTGTTTGTGATGCTGGTCCGCGCCACGCGGCCCTCTACACATGTTAGTGG 630
QY 216 ValThrSerPheLeuPheTyrLeuLeuProMetThrValIleSerValLeuTyrLeu 235
Db 631 ACCACCGCGCTGCTCTTCTTCTGCTGCCATGGCCATCATGAGCGTGTCTACCTGCTC 690
QY 236 MetAlaLeuArgVal 240
Db 691 ATTGGGCTGGGACTG 705
RESULT 7
US-10-083-168-13
; Sequence 13, Application US/10083168
; Publication NO. US20030023069A1
; GENERAL INFORMATION:
; APPLICANT: Liaw, Chen W.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Behan, Dominic P.

; APPLICANT: Maciejewski-Lenior, Dominique
 ; APPLICANT: Leonard, James N.
 ; APPLICANT: Ortuno, Daniel
 ; APPLICANT: Lin, I-lin
 ; TITLE OF INVENTION: Endogenous And No. US20030023069A1-Endogenous, Constitutively Act
 ; TITLE OF INVENTION: Receptors
 ; FILE REFERENCE: AREN-0320
 ; CURRENT APPLICATION NUMBER: US/10/083,168
 ; CURRENT FILING DATE: 2002-02-26
 ; NUMBER OF SEQ ID NOS: 102
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 13
 ; LENGTH: 1212
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-083-168-13

Alignment Scores:
 Pred. No.: 3,32e-70 Length: 1212
 Score: 680.50 Matches: 126
 Percent Similarity: 74.67% Conservative: 42
 Best Local Similarity: 56.00% Mismatches: 54
 Query Match: 53.88% Indels: 3
 DB: 15 Gaps: 2

US-09-684-725-2 (1-242) x US-10-083-168-13 (1-1212)

QY	17	AspProPheGlnLysHisLeuAsnSerThrGluGluTyrLeuAlaPhe---	LeuCysGly	35
DB	37	GACCT-----GAGGACTTGACCTGACGAGGCACTGAGACTCAAGTACCTGGGG		90
QY	36	ProArgGserHisPheLeuProValSerValValTyrValProfilePheValVal		55
DB	91	CCCCAGCAGACAGAGCTGTTTCATGCCCATCTGTGCCACATACCTGCTGTGATCTTCGTGGTG		150
QY	56	GlyValIleGlyAsnValLeuValCysLeuValIleLeuGlnHisGlnAlaMetLysThr		75
DB	151	GGCGCTGTGGCAATGGGCTGACCTGCTGTGTCATCTCGCCACACAGGCACTGGCGCAG		210
QY	76	ProThrAsnTyrTyrLeuPheSerLeuAlaValSerAspLeuLeuValLeuLeuGly		95
DB	211	CTTACCAACTACTACTCTTCAGCTGGCGGTGTGGACCTGCTGGTGCTGTGGTGGGC		270
QY	96	MetProLeuGluValTyrGluMetTyrArgAsnTyrProPheLeuPheGlyProValGly		115
DB	271	CTGCCCCCTGGAGCTCTATGAGATGTGSCAACACTACCCCTCTCTGCTGGGCGTGGTGGC		330
QY	116	CysTyrPheLysThrAlaLeuPheGluThrValCysPheAlaSerIleLeuSerIleThr		135
DB	331	TGCTATTTCGCGACGCTACTGTTTGGATGGTCTGCTGGCCCTCAGTGTCTCAACGTCACT		390
QY	136	ThrValSerValGluArgTyrValAlaIleLeuHisProPheArgAlaLysLeuGlnSer		155
DB	391	GCCCTGAGCGTGAACGCTATGTGGCGTGGTGACCCACTCCAGCGCAGGTCCATGGTG		450
QY	156	ThrArgArgArgAlaLeuArgIleLeuGlyIleValTrpGlyPheSerValLeuPheSer		175
DB	451	ACGGGGCCCATGTGGCCGAGTGTCTGGGGCGTCTGGGGTCTTGGCCATGCTGTGCTCC		510
QY	176	LeuProAsnThrSerIleHisGlyIleLysPheHisTyrPheProAsnGlySerLeuVal		195
DB	511	CTGCCCAACACACAGCTGCACGGCATCGCGCAGCTGCACGTGCCCTCCGGGGCCCCAGT		570
QY	196	ProGlySerAlaThrCysThrValIleLysProMetTrpIleTyrAsnPheIleGln		215
DB	571	CCAGACTCAGCTGTTTCATGCTGGTCCGCCCCACGGGGCCCTCTACAACTGGTAGTCAG		630
QY	216	ValThrSerPheLeuPheTyrLeuLeuProMetThrValIleSerValLeuTyrTyrLeu		235
DB	631	ACCAACGGCGTCTCTTCTTCTGCTGCCCATGGCCCATCATGAGCGTGTCTTACCTGCTC		690
QY	236	MetAlaLeuArgVal		240

Db 511 CTGCCAACACGCTGCAAGGCAATCCGGCACTGCCGTGCCCTGGCGGGCCAGTG 570
Qy 196 ProGlySerAlaThrCysThrValIleLysPheMetTrpIleValPheSerValLeuPheSer 215
Db 571 CCAGACTCAGCTTTGTCATGCTGGTCCGCGCCAGCGCCCTCTACAACTAGTAGTCAG 630
Qy 216 ValThrSerPheLeuPheThrValLeuProMetThrValIleSerValLeuTyrrLeu 235
Db 631 ACCACCGCGTGTCTTCTCTGCTGCCATGCCATCATGAGCGTGTCTACCTGCTC 690
Qy 236 MetAlaLeuArgVal 240
Db 691 ATTGGGCTGGCACTG 705
RESULT 9
US-10-251-385-113
; Sequence 113, Application US/10251385
; Publication No. US20030105292A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human G
; TITLE OF INVENTION: Protein-Coupled
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/10/251,385
; CURRENT FILING DATE: 2002-09-20
; PRIOR FILING DATE: US/09/170,496
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 113
; LENGTH: 1212
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-251-385-113
Alignment Scores:
Pred. No.: 3.32e-70 Length: 1212
Score: 680.50 Matches: 126
Percent Similarity: 74.67% Conservative: 42
Best Local Similarity: 56.00% Mismatches: 54
Query Match: 53.88% Indels: 3
DB: 15 Gaps: 2
US-09-684-725-2 (1-242) x US-10-251-385-113 (1-1212)
Qy 17 AspProPheGlnLysHisLeuAsnSerThrGluTyrLeuAlaPhe---LeuCysGly 35
Db 37 GACCCCT-----GAGGACTTGAACCTGACTGACGAGGCACTGAGACTCAAGTACCTGGGG 90
Qy 36 ProArgArgSerHisPhePheLeuProValSerValValTyrValProIlePheValVal 55
Db 91 CCCAGCAGCAGACGAGCTGTTTCATGCCCATCTGTGCCACATACCTGTGATCTTCGTGGTG 150
Qy 56 GlyValIleGlyAsnValLeuValCysLeuValIleLeuGlnHisGlnAlaMetLysThr 75
Db 151 GCGCTGTGGCAATGGGCTGCTGTGTCATCTCTGCGCCACAGGCCATCGGCAG 210
Qy 76 ProThrAsnTyrTyrLeuPheSerLeuAlaValSerAspLeuLeuValLeuLeuGly 95
Db 211 CCTACCAACTACTACCTCTTCAGCTGGCGGTGCGACCTGCTGTGCTGTGGTGGGC 270
Qy 96 MetProLeuGluValTyrGluMetTyrArgAsnTyrProPheLeuPheGlyProValGly 115
Db 271 CTGCCCTTGAGCTCTATGAGTGTGGCACTACCTCCCTTCCTGTGCGGCTGTGGTGGC 330
Qy 116 CysTyrPheLysThrAlaLeuPheGluThrValCysPheAlaSerIleLeuSerIleThr 135
Db 331 TGCTATTCGCGAGCTACTGTTTGAGTGTGTGCTGCGCTCACTGCTCACTGCTCACT 390
Qy 136 ThrValSerValGluArgTyrValAlaIleLeuHisProPheArgAlaLysLeuGlnSer 155

Db 391 GCCCTGAGCGTGAACGCTATGTGGCGTGTGACCCACTCCAGGCCAGGTCCATGGTG 450
Qy 156 ThrArgArgArgAlaLeuArgIleLeuGlyTleValTrpGlyPheSerValLeuPheSer 175
Db 451 ACGGGGGCCCATGTGCGCCGAGTGTGGGGCGCTCTGGGGCTTTGGCATGCTCTGTCTCC 510
Qy 176 LeuProAsnThrSerIleHisGlyIleLysPheHisTyrPheProAsnGlySerLeuVal 195
Db 511 CTGCCAACACGAGCTGCAAGGCAATCCGGCACTGCCGTGCCCTGGCGGGCCAGTG 570
Qy 196 ProGlySerAlaThrCysThrValIleLysPheMetTrpIleValPheSerValLeuTyrrLeu 215
Db 571 CCAGACTCAGCTTTGTCATGCTGGTCCGCGCCAGCGCCCTCTACAACTAGTAGTCAG 630
Qy 216 ValThrSerPheLeuPheThrValLeuProMetThrValIleSerValLeuTyrrLeu 235
Db 631 ACCACCGCGTGTCTTCTCTGCTGCCATGCCATCATGAGCGTGTCTACCTGCTC 690
Qy 236 MetAlaLeuArgVal 240
Db 691 ATTGGGCTGGCACTG 705
RESULT 10
US-10-251-385-223
; Sequence 223, Application US/10251385
; Publication No. US20030105292A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. US20030105292A1-Endogenous, Constitutively Activated Human G
; TITLE OF INVENTION: Protein-Coupled
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/10/251,385
; CURRENT FILING DATE: 2002-09-20
; PRIOR FILING DATE: US/09/170,496
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 223
; LENGTH: 1212
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-251-385-223
Alignment Scores:
Pred. No.: 3.32e-70 Length: 1212
Score: 680.50 Matches: 126
Percent Similarity: 74.67% Conservative: 42
Best Local Similarity: 56.00% Mismatches: 54
Query Match: 53.88% Indels: 3
DB: 15 Gaps: 2
US-09-684-725-2 (1-242) x US-10-251-385-223 (1-1212)
Qy 17 AspProPheGlnLysHisLeuAsnSerThrGluTyrLeuAlaPhe---LeuCysGly 35
Db 37 GACCCCT-----GAGGACTTGAACCTGACTGACGAGGCACTGAGACTCAAGTACCTGGGG 90
Qy 36 ProArgArgSerHisPhePheLeuProValSerValValTyrValProIlePheValVal 55
Db 91 CCCAGCAGCAGACGAGCTGTTTCATGCCCATCTGTGCCACATACCTGTGATCTTCGTGGTG 150
Qy 56 GlyValIleGlyAsnValLeuValCysLeuValIleLeuGlnHisGlnAlaMetLysThr 75
Db 151 GCGCTGTGGCAATGGGCTGACCTGTGTCATCTCTGCGCCACAGGCCATCGGCAG 210
Qy 76 ProThrAsnTyrTyrLeuPheSerLeuAlaValSerAspLeuLeuValLeuLeuGly 95
Db 211 CCTACCAACTACTACTACCTCTTCAGCTGGCGGTGCGACCTGCTGTGCTGTGGTGGGC 270

; PRIOR APPLICATION NUMBER: NOT YET ASSIGNED ; PRIOR FILING DATE: 2000-03-14 ; NUMBER OF SEQ ID NOS: 172 ; SOFTWARE: Custom ; SEQ ID NO 96 ; LENGTH: 1349 ; TYPE: DNA ; ORGANISM: Homo sapiens ; US-10-240-145-96		; APPLICANT: Hyseq, Inc ; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES ; FILE REFERENCE: 21272-048 ; CURRENT APPLICATION NUMBER: US/10/240,145 ; CURRENT FILING DATE: 2002-09-27 ; PRIOR APPLICATION NUMBER: 09/540,217 ; PRIOR FILING DATE: 2000-03-31 ; PRIOR APPLICATION NUMBER: 09/649,167 ; PRIOR FILING DATE: 2000-08-23 ; PRIOR APPLICATION NUMBER: 09/668,680 ; PRIOR FILING DATE: 2000-09-22 ; PRIOR APPLICATION NUMBER: 09/695,618 ; PRIOR FILING DATE: 2000-10-23 ; PRIOR APPLICATION NUMBER: 09/728,711 ; PRIOR FILING DATE: 2000-11-30 ; PRIOR APPLICATION NUMBER: NOT YET ASSIGNED ; PRIOR FILING DATE: 2000-03-14 ; NUMBER OF SEQ ID NOS: 172 ; SOFTWARE: Custom ; SEQ ID NO 10 ; LENGTH: 1535 ; TYPE: DNA ; ORGANISM: Homo sapiens ; FEATURE: ; NAME/KEY: CDS ; LOCATION: (1)..(1335) ; US-10-240-145-10	
Alignment Scores: Pred. No.: 8,83e-70 Length: 1349 Score: 677.50 Matches: 126 Percent Similarity: 74.22% Conservative: 41 Best Local Similarity: 56.00% Mismatches: 55 Query Match: 53.64% Indels: 3 DB: 12 Gaps: 2		Alignment Scores: Pred. No.: 1,07e-69 Length: 1535 Score: 677.50 Matches: 126 Percent Similarity: 74.22% Conservative: 41 Best Local Similarity: 56.00% Mismatches: 55 Query Match: 53.64% Indels: 3 DB: 12 Gaps: 2	
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Qy	17 AspProPheGlnLysHisLeuAsnSerThrGluGluTyrLeuAlaPhe---LeuCysGly	Qy	17 AspProPheGlnLysHisLeuAsnSerThrGluGluTyrLeuAlaPhe---LeuCysGly
Db	163 GACCCCT-----GAGGACTTGAACCTGACTGACGAGGCACCTGAGACTCAAGTACTGGGG	Db	163 GACCCCT-----GAGGACTTGAACCTGACTGACGAGGCACCTGAGACTCAAGTACTGGGG
Qy	36 ProArgArgSerHisPhePheLeuProValSerValValTyrValProIlePheValVal	Qy	36 ProArgArgSerHisPhePheLeuProValSerValValTyrValProIlePheValVal
Db	217 CCCACGACGAGAGCTGTTCACTGCCCATCTGTGCCACATACCTGCTGATCTTCTGTGTG	Db	217 CCCACGACGAGAGCTGTTCACTGCCCATCTGTGCCACATACCTGCTGATCTTCTGTGTG
Qy	56 GlyValIleGlyAsnValLeuValCysLeuValIleLeuGlnHisGlnAlaMetLysThr	Qy	56 GlyValIleGlyAsnValLeuValCysLeuValIleLeuGlnHisGlnAlaMetLysThr
Db	277 GCGCGTGTGGCAATGGGTGACCTGTCTGTGTCATCTTCCGCGCCACAGGCATCGGCACG	Db	277 GCGCGTGTGGCAATGGGTGACCTGTCTGTGTCATCTTCCGCGCCACAGGCATCGGCACG
Qy	76 ProThrAsnTyrTyrLeuPheSerLeuAlaValSerAspLeuValLeuLeuGly	Qy	76 ProThrAsnTyrTyrLeuPheSerLeuAlaValSerAspLeuValLeuLeuGly
Db	337 CCTACCAACTACTACTCTTTCAGCTGGCGGTGTCGGACCTGCTGCTGCTGTGTGGGG	Db	337 CCTACCAACTACTACTCTTTCAGCTGGCGGTGTCGGACCTGCTGCTGCTGTGTGGGG
Qy	96 MetProLeuGluValTyrGluMetTrpArgAsnTyrProPheLeuPheGlyProValGly	Qy	96 MetProLeuGluValTyrGluMetTrpArgAsnTyrProPheLeuPheGlyProValGly
Db	397 CTGCGCTGTGGCAATGGGTGACCTGTCTGTGTCATCTTCCGCGCCACAGGCATCGGCACG	Db	397 CTGCGCTGTGGCAATGGGTGACCTGTCTGTGTCATCTTCCGCGCCACAGGCATCGGCACG
Qy	116 CysTyrPheLysThrAlaLeuPheGluThrValCysPheAlaSerIleLeuSerIleThr	Qy	116 CysTyrPheLysThrAlaLeuPheGluThrValCysPheAlaSerIleLeuSerIleThr
Db	457 TGTATTTCCGACGCTACTGTTTGAGATGGTCTGCGGCGCTGCGGCTCTGCTGCTGCTC	Db	457 TGTATTTCCGACGCTACTGTTTGAGATGGTCTGCGGCGCTGCGGCTCTGCTGCTGCTC
Qy	136 ThrValSerValGluArgTyrValAlaIleLeuHisProPheArgAlaLysLeuGlnSer	Qy	136 ThrValSerValGluArgTyrValAlaIleLeuHisProPheArgAlaLysLeuGlnSer
Db	517 GCCTGTGGCGTGGAAACGCTATGTGGCGGTGGTGACCCACCTCCAGGCCAGGTCCATGGTG	Db	517 GCCTGTGGCGTGGAAACGCTATGTGGCGGTGGTGACCCACCTCCAGGCCAGGTCCATGGTG
Qy	156 ThrArgArgArgAlaLeuArgIleLeuGlyIleValTrpGlyPheSerValLeuPheSer	Qy	156 ThrArgArgArgAlaLeuArgIleLeuGlyIleValTrpGlyPheSerValLeuPheSer
Db	577 ACGGGGCCCATGTGCGCGAGTGTCTTGGGGCGGTCTTGGGGTCTTGGCATCTCTGCTCC	Db	577 ACGGGGCCCATGTGCGCGAGTGTCTTGGGGCGGTCTTGGGGTCTTGGCATCTCTGCTCC
Qy	176 LeuProAsnThrSerIleHisGlyIleValTrpGlyPheSerValLeuPheSer	Qy	176 LeuProAsnThrSerIleHisGlyIleValTrpGlyPheSerValLeuPheSer
Db	637 CTGCCCAACACGAGCTGTGACGCGCTGCGGCTGCGGAGTGTGCTGCTGCTGCTGCTGCTG	Db	637 CTGCCCAACACGAGCTGTGACGCGCTGCGGCTGCGGAGTGTGCTGCTGCTGCTGCTGCTG
Qy	196 ProGlySerAlaThrCysThrValIleLysProMetTrpIleTyrAsnPheIleIleGln	Qy	196 ProGlySerAlaThrCysThrValIleLysProMetTrpIleTyrAsnPheIleIleGln
Db	697 CCAGACTCAGCTGTTTGTGATGTGGTGGCGCCGACGCGGCGCTCTCAACATGTGTGCG	Db	697 CCAGACTCAGCTGTTTGTGATGTGGTGGCGCCGACGCGGCGCTCTCAACATGTGTGCG
Qy	216 ValThrSerPheLeuPheTyrLeuLeuProMetThrValIleSerValLeuTyrLeu	Qy	216 ValThrSerPheLeuPheTyrLeuLeuProMetThrValIleSerValLeuTyrLeu
Db	757 ACCACCGCGTGTCTTCTTCTGCTGCCATGGCCATCATGAGGCGTGTCTTCTTCTGCTC	Db	757 ACCACCGCGTGTCTTCTTCTGCTGCCATGGCCATCATGAGGCGTGTCTTCTTCTGCTC
Qy	236 MetAlaLeuArgVal 240	Qy	236 MetAlaLeuArgVal 240
Db	817 ATTGGGCTGGGACTG 831	Db	817 ATTGGGCTGGGACTG 831
RESULT 15 US-10-240-145-10 ; Sequence 10, Application US/10240145 ; Publication No. US20030235883A1 ; GENERAL INFORMATION:		RESULT 15 US-10-240-145-10 ; Sequence 10, Application US/10240145 ; Publication No. US20030235883A1 ; GENERAL INFORMATION:	

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QY 196 ProGlySerAlaThrCysThrValIleLysProMetTyrPileTyrAsnPheIleIleGln 215
Db 697 CCAGACTCAGCTGTTGTCATGCTGGTCCCGCCACGGGCCCTCTACACATGGTAGTGCAG 756

QY 216 ValThrSerPheLeuPheTyrLeuLeuProMetThrValIleSerValLeuTyrTyrLeu 235
Db 757 ACCACCGCGCTGCTCTTCTGCTGCCCATGGCCATCATGAGCGTGTCTACCTGCTC 816

QY 236 MetAlaLeuArgVal 240
Db 817 ATGGGCTGCGACTG 831

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Search completed: February 16, 2004, 09:20:45
Job time : 333 secs